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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/890,646

DATE: 01/03/2002
TIME: 21:57:13

Input Set: I890646.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: AYABE, SHINICHI
2 AOKI, TOSHIO
3 AKASHI, TOMOYOSHI
4 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE SYNTHASE
5 <130> FILE REFERENCE: JKM-001
6 <140> CURRENT APPLICATION NUMBER: US/09/890,646
7 <141> CURRENT FILING DATE: 2001-08-02
8 <150> EARLIER APPLICATION NUMBER: PCT/JP00/00596
9 <151> EARLIER FILING DATE: 2000-02-04
10 <160> NUMBER OF SEQ ID NOS: 14
11 <170> SOFTWARE: PatentIn Ver. 2.1
12 <210> SEQ ID NO 1
13 <211> LENGTH: 1895
14 <212> TYPE: DNA
15 <213> ORGANISM: Glycyrrhiza echinata
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (144)..(1712)
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20 cacaaatcct aattgccctc aactcataaa tctctccagg tactggactc ttgttcctgt 60
21 acttcctcct atactcgact ctttggttatt agttatcatt attattatta caccattaaa 120
22 gtagcaaaga tcaaacaaac acc atg ttg gtg gaa ctt gca att act ctg ttg 173
23 Met Leu Val Glu Leu Ala Ile Thr Leu Leu
24 1 5 10
25 gtg ata gcc ctg ttc ata cac ctg cgt ccc aca cta agt gca aaa tca 221
26 Val Ile Ala Leu Phe Ile His Leu Arg Pro Thr Leu Ser Ala Lys Ser
27 15 20 25
28 aag tcc ctt cgc cac ctg cca aac cct cca agt cca aaa ccc cgt ctg 269
29 Lys Ser Leu Arg His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu
30 30 35 40
31 cca ttt gtg ggt cac ctt cac ctt tta gac aaa ccc ctt ctg cac tac 317
32 Pro Phe Val Gly His Leu His Leu Leu Asp Lys Pro Leu Leu His Tyr
33 45 50 55
34 tcc ctg atc gac cta agc aaa cgc tat ggt ccg ctt tac tcc ctg tac 365
35 Ser Leu Ile Asp Leu Ser Lys Arg Tyr Gly Pro Leu Tyr Ser Leu Tyr
36 60 65 70
37 ttc ggt tcc atg cca acc gtt gta gcc tcc acc cct gaa ctt ttc aaa 413
38 Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys
39 75 80 85 90
40 ctg ttc ctg caa act cac gag gcc tct tcc ttc aac aca agg ttc caa 461
41 Leu Phe Leu Gln Thr His Glu Ala Ser Ser Phe Asn Thr Arg Phe Gln
42 95 100 105
43 acc tct gcc att agg cgc cta acc tac gac aac tct gtt gcc atg gtt 509
44 Thr Ser Ala Ile Arg Arg Leu Thr Tyr Asp Asn Ser Val Ala Met Val

45																			
46	ccc	ttt	ggt	cct	tac	tgg	aag	ttc	att	agg	aag	ctc	atc	atg	aac	gac		557	
47	Pro	Phe	Gly	Pro	Tyr	Trp	Lys	Phe	Ile	Arg	Lys	Leu	Ile	Met	Asn	Asp			
48				125				130					135						
49	ctc	ctc	aat	gcc	aca	act	gtg	aac	aag	ttg	agg	cct	tta	agg	agc	caa		605	
50	Leu	Leu	Asn	Ala	Thr	Thr	Val	Asn	Lys	Leu	Arg	Pro	Leu	Arg	Ser	Gln			
51			140					145					150						
52	gaa	atc	cga	aag	gtc	ctc	agg	gtg	atg	gca	cag	agt	gct	gag	tct	cag		653	
53	Glu	Ile	Arg	Lys	Val	Leu	Arg	Val	Met	Ala	Gln	Ser	Ala	Glu	Ser	Gln			
54	155						160				165					170			
55	gtc	cca	ctt	aat	gtc	acc	gag	gag	ctt	ctc	aag	tgg	acc	aac	agc	acc		701	
56	Val	Pro	Leu	Asn	Val	Thr	Glu	Glu	Leu	Leu	Lys	Trp	Thr	Asn	Ser	Thr			
57					175					180					185				
58	atc	tcg	agg	atg	atg	ctt	ggg	gaa	gca	gag	gaa	atc	agg	gac	ata	gca		749	
59	Ile	Ser	Arg	Met	Met	Leu	Gly	Glu	Ala	Glu	Glu	Ile	Arg	Asp	Ile	Ala			
60				190					195					200					
61	cgt	gac	gtg	ctt	aag	atc	ttt	ggg	gag	tat	agt	ctc	acc	gac	ttc	atc		797	
62	Arg	Asp	Val	Leu	Lys	Ile	Phe	Gly	Glu	Tyr	Ser	Leu	Thr	Asp	Phe	Ile			
63			205					210					215						
64	tgg	ccc	ttg	aag	aaa	ctc	aag	gtt	ggg	caa	tac	gag	aag	agg	att	gac		845	
65	Trp	Pro	Leu	Lys	Lys	Leu	Lys	Val	Gly	Gln	Tyr	Glu	Lys	Arg	Ile	Asp			
66		220					225					230							
67	gat	ata	ttc	aac	agg	ttt	gac	ccc	gtc	att	gag	agg	gtc	atc	aag	aaa		893	
68	Asp	Ile	Phe	Asn	Arg	Phe	Asp	Pro	Val	Ile	Glu	Arg	Val	Ile	Lys	Lys			
69	235					240					245					250			
70	aga	cag	gag	att	agg	aag	aag	agg	aag	gag	agg	aat	ggt	gag	atc	gag		941	
71	Arg	Gln	Glu	Ile	Arg	Lys	Lys	Arg	Lys	Glu	Arg	Asn	Gly	Glu	Ile	Glu			
72				255					260						265				
73	gag	ggt	gaa	cag	agt	gtg	gtt	ttt	ctc	gac	act	ttg	ctc	gat	ttt	gct		989	
74	Glu	Gly	Glu	Gln	Ser	Val	Val	Phe	Leu	Asp	Thr	Leu	Leu	Asp	Phe	Ala			
75			270					275					280						
76	gag	gac	gag	acc	atg	gag	atc	aaa	atc	acc	aag	gaa	caa	atc	aag	ggc		1037	
77	Glu	Asp	Glu	Thr	Met	Glu	Ile	Lys	Ile	Thr	Lys	Glu	Gln	Ile	Lys	Gly			
78			285					290					295						
79	ctt	gtt	gtg	gat	ttc	ttc	tca	gca	ggg										

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95      Val Gln Glu Cys Glu Val Asp Gly Tyr Val Ile Pro Glu Gly Ala Leu
96          380                      385                      390
97      atc ctt ttc aat gtt tgg gcc gtc gga aga gac cca aaa tac tgg gac      1373
98      Ile Leu Phe Asn Val Trp Ala Val Gly Arg Asp Pro Lys Tyr Trp Asp
99      395                      400                      405                      410
100     agg ccc act gag ttc cgt ccc gaa agg ttc tta gaa aat gtg ggt gaa      1421
101     Arg Pro Thr Glu Phe Arg Pro Glu Arg Phe Leu Glu Asn Val Gly Glu
102                      415                      420                      425
103     ggg gat caa gcc gtt gac ctt agg ggt caa cat ttc caa ctt ctt ccg      1469
104     Gly Asp Gln Ala Val Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro
105                      430                      435                      440
106     ttt ggg tct gga agg agg atg tgc cct ggc gtc aat ttg gcc act gcg      1517
107     Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ala
108                      445                      450                      455
109     gga atg gcc aca ctg ctt gcg tca gtt atc cag tgc ttt gat ctc agc      1565
110     Gly Met Ala Thr Leu Leu Ala Ser Val Ile Gln Cys Phe Asp Leu Ser
111                      460                      465                      470
112     gta gtg ggc cca cag gga aag ata ttg aag ggc aat gat gcc aag gtt      1613
113     Val Val Gly Pro Gln Gly Lys Ile Leu Lys Gly Asn Asp Ala Lys Val
114     475                      480                      485                      490
115     agc atg gaa gag aga gct gga ctc acg gtt cca agg gca cat aac ctc      1661
116     Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala His Asn Leu
117                      495                      500                      505
118     atc tgt gtc ccg gtt gca aga tca agt gcc gta ccc aaa ctc ttt tcg      1709
119     Ile Cys Val Pro Val Ala Arg Ser Ser Ala Val Pro Lys Leu Phe Ser
120                      510                      515                      520
121     tcg taaaacatac gcgcgacacc agaaagctgc catggcatga tgctttttat      1762
122     Ser
W--> 123
124     ataataattt tcaataaggt atcaatcaat gatatataga caatgatacc catatatcat      1822
125     ctctcgact agtctctctt tggtagagta tgttgtaaca gcttaaactt atataatttt      1882
126     tactgcata tcc      1895
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128     <211> LENGTH: 523
129     <212> TYPE: PRT
130     <213> ORGANISM: Glycyrrhiza echinata
131     <400> SEQUENCE: 2
132     Met Leu Val Glu Leu Ala Ile Thr Leu Leu Val Ile Ala Leu Phe Ile
133     1                      5                      10                      15
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135     20                      25                      30
136     Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Val Gly His Leu
137     35                      40                      45
138     His Leu Leu Asp Lys Pro Leu Leu His Tyr Ser Leu Ile Asp Leu Ser
139     50                      55                      60
140     Lys Arg Tyr Gly Pro Leu Tyr Ser Leu Tyr Phe Gly Ser Met Pro Thr
141     65                      70                      75                      80
142     Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
143     85                      90                      95
144     Glu Ala Ser Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg

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196      Arg Ser Ser Ala Val Pro Lys Leu Phe Ser Ser
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199      <211> LENGTH: 422
200      <212> TYPE: DNA
201      <213> ORGANISM: Glycyrrhiza echinata
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205      caaggttagc atggaagaga gagctggact cacggttcca agggcacata acctcatctg 180
206      tgtcccgggtt gcaagatcaa gtgccgtacc caaactcttt tcgtcgtaaa acatacgcgc 240
207      gacaccacag aaagttgcc a tggcatgatg ctttttatat aataattttc aataagggtat 300
208      caatcaatga tatatagaca atgataccca tatatcatct tcacgactag tctctctttg 360
209      gtacagtatg ttgtaacagc ttaaattctat ataattttta ctcgcatatc catttcctga 420
210      tt 422
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212      <211> LENGTH: 28
213      <212> TYPE: DNA
214      <213> ORGANISM: Artificial Sequence
215      <220> FEATURE:
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220      <211> LENGTH: 29
221      <212> TYPE: DNA
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223      <220> FEATURE:
224      <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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230      <213> ORGANISM: Artificial Sequence
231      <220> FEATURE:
232      <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
233      <400> SEQUENCE: 6
234      Leu Pro Phe Gly Ser Gly Arg Arg Ser Cys
235      1 5 10
236      <210> SEQ ID NO 7
237      <211> LENGTH: 12
238      <212> TYPE: PRT
239      <213> ORGANISM: Artificial Sequence
240      <220> FEATURE:
241      <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
242      <400> SEQUENCE: 7
243      Tyr Leu Gln Ala Ile Val Lys Glu Thr Leu Arg Leu
244      1 5 10

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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text

123 W Invalid/Missing Amino Acid Numbering

272 W "N" or "Xaa" used: Feature required

htnscnttyr gnnnnggnms nmg